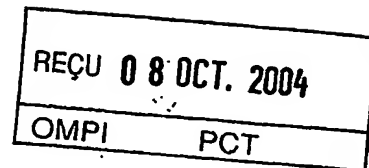


PCT/1504/10



# LÝÐVELDIÐ ÍSLAND

*Hér með staðfestist að meðfylgjandi eru rétt afrit af gögnum sem upphaflega voru lögð inn hjá Einkaleyfastofunni vegna neðargreindrar einkaleyfisumsóknar.*

This is to certify that the annexed is a true copy of the documents as originally filed with the Icelandic Patent Office in connection with the following patent application.

(21) *Umsóknarnúmer*  
Patent application number

6929

(71) *Umsækjandi*  
Applicant(s)

ORF Líftækni ehf.

(22) *Umsóknardags.*  
Date of filing

27.8.2003

**PRIORITY  
DOCUMENT**  
SUBMITTED OR TRANSMITTED IN  
COMPLIANCE WITH RULE 17.1(a) OR (b)



**E/S**  
**EINKALEYFASTOFAN**

Reykjavík, 30. september 2004

*Páll R. Johannesson*  
Páll Ragnar Johannesson  
Patent Division

## A PROCESS TO PURIFY RECOMBINANT PROTEINS FROM PLANTS

### FIELD OF THE INVENTION

- 5 The present invention is in the area of biochemistry and protein technology and relates to improved methods of isolation and purification of heterologous proteins from transgenic plant material. Furthermore, the present invention presents an improved and economical way of proteolytic cleavage of fusion proteins.

### 10 BACKGROUND

Protein based biopharmaceuticals show great promise in providing more specific and tissue specific, or cell specific drug treatments against serious diseases (for overview see "Recombinant Protein Drugs" Ed. P. Buckel 2001).

15

Many examples in the literature have demonstrated the utilization of transgenic plants or plant cell cultures for expression and manufacturing of high-value heterologous polypeptides or biopharmaceuticals. Such plant-based manufacturing process may be called molecular farming.

20

Production of valuable proteins can be made more economical by the use of plants as production organisms. The cultivation cost for plants used as host organisms for protein manufacturing can be considerably lower compared to most production systems based on bioreactors, such as prokaryotic production systems, animal cell cultivation and so forth. However, for all of the above

25 production systems, purification of heterologous proteins remains a demanding task. Thus, for plant-based production systems, downstream processing generates most of the production costs in the manufacturing of high-value heterologous proteins.

30

Protein purification and isolation is a key process in downstream processing of proteins accumulated and produced in a variety of host organisms by the use of gene technology. The purification of proteins from the host organisms can be quite laborious, complex and expensive. A variety of chromatographic strategies

35 are used commercially for separation and purification of proteins of interest from production host organisms. The chromatographic strategies may rely on physicochemical differences between contaminating or endogenous proteins and

the heterologous protein of interest, such as in size, solubility, charge, hydrophobicity, and affinity.

Combinations of chromatographic strategies consisting of multiple steps, require several expensive chromatography matrices and the necessary hardware

5 consisting of columns, control units and so forth, and are accompanied by product yield-losses at each step, and consequently, economical losses. In addition to the chromatographic steps involved, downstream processing typically involves multiple filtering and centrifugation steps. As a result, the cost of purification and downstream processing may become prohibitive for the purification of a protein  
10 based biotechnological product. As for a number of protein-based products of lesser value, such as industrial proteins, the cost of downstream processing can be inhibitory for their use and marketing, resulting in crude and poorly defined products. For most biotechnology products purification costs are certainly a major proportion of the manufacturing costs.

15 The cost of specialized chromatography matrices effecting the separation of a protein of interest from contaminants is high as a result of complex coupling chemistry involved in their production. Some common chromatography methods are ion exchange chromatography, hydrophobic interaction chromatography and  
20 reversed phase chromatography. Ligands coupled to a matrices may include a variety of diethylaminoethyl- or quaternary aminoethyl groups as anion exchangers and carboxymethyl substituents and sulfonate groups and phosphates as cation exchangers of varying strength (Scopes, 1993), hydrophobic alkyl, phenyl or butyl groups coupled to crosslinked agarose matrices for hydrophobic  
25 interaction chromatography (Hydrophobic Interaction Chromatography (HIC) nr. 18-1020-90, Amersham Pharmacia Biotech), or hydrophobic n-alkyl groups as ligands grafted to a porous, insoluble beaded matrices composed of silica or synthetic organic polymers (Reversed phase Chromatography (RPC), Code nr. 18-11134-16, Amersham Pharmacia Biotech) The chemical complexity of these  
30 matrices may cause unwanted leaching of ligands and other substances from the matrix during a purification procedure, where necessary preventive measures, monitoring, or the removal of leachates from the protein of interest add to the already high cost of downstream processing.

35 Affinity chromatography is among the most powerful purification principles as it is based on specific affinity between an agent and a specific ligand, often mimicking a natural protein-ligand interaction. Several different kinds of affinity adsorbents are available, some highly specific for a particular protein, others binding to

classes of proteins rather than particular proteins. In many cases affinity chromatography implies the use of an immobilized ligand to an adsorbent that specifically selects out proteins binding to that ligand. The coupling of ligands to affinity adsorbents involves the use of coupling chemistry such as cyanogen

5 bromide-, tosyl-, or vinylsulfone-activation of adsorbents. The ligand coupled to the column matrix may or may not be of proteinaceous origin. Examples of the former are, but not limited to, immobilized protein A or protein G having affinity for  $\gamma$ -globulin, therefore being useful in the purification of antibodies, and lectins with affinity for glycoproteins. As an example of the latter, immobilized  
10 glutathione coupled to matrix binds fusion proteins containing a glutathione S-transferase domain. Immobilized metal affinity chromatography (IMAC) is based on immobilization of metal-chelating ligands to a matrix and relies on the formation of weak coordinate bonds between metal ions immobilized on a column and basic groups on proteins, mainly histidine residues. Commercial cloning  
15 vectors provide for cloning of a cDNA in frame with a string of histidine residues – a his-tag, that enables the purification of the resultant fusion protein with IMAC. Although widely used for small-scale purification of proteins, IMAC is a non-specific but selective method, as native histidine residues in contaminating proteins can lead to binding in IMAC (Scopes 1993). Several different kinds of  
20 tags or binding domains are available in commercial expression vectors resulting in fusion proteins where the tag/binding domain binds the fusion protein to a coupled ligand on a column matrix.

High specificity of protein binding can be achieved with these matrix-ligand systems. In the cases mentioned above, complex coupling chemistry is involved  
25 to immobilize a ligand onto an inert matrix. Consequently, the cost of an affinity matrix can often become inhibitory to industrial scale applications of this powerful technique.

Furthermore, as with most other types of chromatography methods, the stability of the coupling of the ligand to the matrix becomes an issue and leaching is of  
30 great concern. Heavy metal leaching in IMAC can cause unacceptable and serious contamination in many sensitive purification processes for bioactive proteins, and may inactivate proteins being purified (Scopes 1993).

It is not uncommon that the binding affinity of a protein to its ligand is so strong that conditions for elution, to disrupt the ligand-protein binding require drastic  
35 conditions that partly denature the valuable protein being purified. A non-limiting example of this is the elution of antibodies from Protein A-affinity matrix, requiring denaturing at low pH to release the antibody from the column. Including a denaturing step in a protein purification process is undesirable due to the risk of

loss of activity of the purified protein, the addition of an extra step for refolding the protein and subsequent activity analysis requirements for the refolded protein product, and the added cost involved.

- 5 To enable the use of affinity-based chromatography for large scale purification from plants, it is highly desirable to develop a purification process that is simpler and more economic than the current measures commercially available, with less coupling chemistry involved and compatible with the quality requirements of the pharmaceutical industry standards.

10

Plant-based production of proteins shows great promise for large scale manufacturing of proteins in an economic manner, as has been shown by examples in literature (for overview see Hammond 1999).

- 15 The cultivation costs involved in molecular farming with plants are considerably lower than with traditional bioreactor-based methods.

Polysaccharides and polysaccharide binding proteins may be used in conjunction for the design of an affinity chromatography step (see, e.g., Boraston et al., 2001).

20

U.S. Patent No. 6,331,416 by Shani et al. describes a method of expressing a recombinant protein with a polysaccharide binding domain that binds to the cellulose in the host plant cell walls, and a protein purification process utilizing the affinity of this protein to host plant cellulose, resulting in a cell wall-protein complex that can be separated from soluble contaminating proteins. The strength of binding can be such that releasing the protein from the cellulosic host plant matter may require drastic conditions that denature the protein, having negative effects on the activity of the recombinant proteins being purified. The complications involved are comparable to those mentioned above for antibody-Protein A elution.

30

The carbohydrate binding domain CBM9-2 is from the *Thermatoga maritima* Xylanase 10A (Winterhalter et al 1995: Mol. Microbiol. 15 (3), 431-444). The CBM9-2 genomic DNA sequence is available as GenBank Accession No. Z46264 and it belongs to the Family IX of CBM-s and has number of attractive properties for high-resolution affinity purification, including non-denaturing eluting conditions using 1M glucose as a eluent, and high specific affinity for amorphous

35

as well as crystalline celluloses (Boraston et al. 2001: Biochemistry 40, 6240-6247).

- 5 There is a recognized need for a downstream process for purification of heterologous proteins from transgenic plant material that is efficient, simple, and economical. Furthermore, there is a need for such a downstream process consisting of gentle, non-denaturing conditions for the protein of interest, (in particular, specific affinity purification methods with gentle elution conditions) in order to secure bioactivity of the protein of interest, and improve yields.
- 10 A protein purification process free from the limitations detailed above could significantly lower the production cost involved in the production of biopharmaceuticals from plants, and would be enabling for the purification of heterologous proteins of value for which downstream processing has been
- 15 prohibitively complex and costly.

#### SUMMARY AND OBJECTS OF THE INVENTION

- 20 The primary objective of present invention is to provide an improved method for protein purification of high-value heterologous proteins produced in plants, plant derived tissue or plant cells.
- The invention aims to reduce the cost and improve the quality of downstream processing of heterologous proteins produced in plants.
- 25
- An important step in the purification process is the separation of the protein of interest as a CBM-fusion protein from cell-wall fragments and other poorly defined plant-derived solids. This can be done separately prior to an affinity chromatography step or simultaneously with an affinity chromatography step.
- 30
- In a first aspect, the invention provides a method for production and purification of a soluble heterologous fusion protein comprising a cellulose binding module (CBM), from transgenic plants or transgenic plant cells expressing said fusion protein, the method comprising:
- 35
- disrupting the transgenic plant material;

adding an extraction liquid to the plant material, thereby creating a mixture of soluble and insoluble plant material, so as to extract the soluble fusion protein from said disrupted plant material to the liquid phase to obtain a protein extract;

5 separating the insoluble plant material, comprising cell-wall material and solids, from said protein extract comprising said fusion protein of interest;

contacting said protein extract to a polysaccharide matrix which binds to said fusion protein;

10 washing the matrix with the bound fusion protein with one or more suitable aqueous solutions such as one or more buffer solutions, i.e., the washing may be preformed in one step, with a gradient or as a sequence of different washing solutions; and

eluting the fusion protein from said polysaccharide matrix by adjusting conditions effecting the release of said fusion protein from the matrix.

15 Typically, the transgenic plant or plant cell is selected from the group of dicotyledonous plants and monocotyledonous plants, and in preferred embodiments said plant cell or transgenic plant is from the group of tobacco, rape seed, soy bean, alfalfa, barley, maize, wheat, oat and rice.

20 The separation step comprises in some embodiments a method selected from expanded bed adsorption (EBA), precipitation, filtration, centrifugation, or any combination thereof.

25 The affinity binding step binding the fusion protein to a polysaccharide matrix preferably comprises a chromatography step.

30 However, in certain useful embodiments, said separation of cell-wall fragments and other poorly defined plant-derived solids from the protein of interest – the CBM-fusion protein, and the affinity binding of the CBM fusion protein to a polysaccharide matrix can be done in a single powerful purification step using Expanded Bed Adsorption chromatography (EBA) with a suitable, inexpensive polysaccharide matrix. This feature streamlines and improves the economy of the downstream processing.

35 In advantageous embodiments of the present invention, the polysaccharide matrix comprises cellulose, and preferably pharmaceutically compatible cellulose.

Such a well-defined pharmaceutical grade cellulosic matrix to which the CBM-fusion protein binds allows various high-end uses of the purified heterologous protein. A useful pharmaceutically compatible cellulose material for use as the polysaccharide matrix comprises Avicel™ (FMC Corporation, PA, USA).

5

The polysaccharide matrix used for affinity chromatography according to the invention requires no complex coupling chemistry or immobilization of potentially leaching ligands. The polysaccharide matrix provides both structural support and rigidity while constituting the affinity adsorbent itself. Thereby, more economical and safer protein purification is enabled for plant derived heterologous proteins.

10

It is still an advantage of this invention that the process described is amenable for different polysaccharide matrices of differing qualities all according to the different end-use of the purified heterologous proteins e.g. in for example agriculture, chemical industry or pharmaceutical industry. An affinity adsorbent made out of polysaccharide of pharmaceutical grade is a bulk material within the pharmaceutical industry and is considerably less expensive than any commercially available affinity chromatography media. Thus, an affinity matrix of very high quality can be made economical using the process described by this invention, enabling more economical downstream processing of high-value proteins from plant derived material.

15

20

It is a further advantage of the present invention that once the plant derived CBM-fusion protein is bound to the polysaccharide chromatography matrix, and after washing the matrix to remove any contaminating endogenous plant proteins, the fusion protein can be eluted from the column using non-denaturing, mild conditions typically neutral or acidic conditions and preferably with the addition of soluble carbohydrates (sugars), that preserve the activity and structure of any fusion partner protein attached to CBM. The sugars compete with the CBM for the binding sites and a suitable concentration will release substantially all of the bound CBM fusion protein.

25

30

It follows that the preferred CBM-s that are used in the methods of the invention and fused to the heterologous protein of interest are such CBM-s that have desired binding characteristics to allow sufficiently strong binding to a suitable polysaccharide matrix to obtain a high yield of bound CBM fusion protein, and releasing by such mild conditions as described above. CBM9-2 has been found to have these desired characteristics. The use of other CBM-s with such

35



characteristics is also within the scope of the invention. Such CBM-s may be found e.g. by searching available gene databases for sequences encoding CBM having desired characteristics, e.g. sequence motifs found to be similar to motifs in CBM9-2 that are important for the binding characteristics. Also, existing CBM-s may be modified with point mutation techniques well known in the art to modify their binding characteristics in order to obtain suitable CBM-s according to the invention.

After the fusion protein has been eluted from the polysaccharide affinity matrix it may optionally be subjected to one or more further purification or isolation steps, depending on the desired form and use of the protein.

In useful embodiments, the transgenic plant or plant cell comprises a nucleic acid sequence encoding for a CBM, preferably the CBM is heat-stable and remains soluble at elevated temperatures. The term heat-stable in this context indicates that the protein remains soluble, correctly folded and active at elevated temperatures, i.e. temperatures above about 25°C, and typically above about 37°C, including the range of 40°C -100°C.

Genes encoding such preferred CBM may be obtained from thermophilic organisms, including thermophilic bacteria, algae and fungus and introduced into the host plant or plant cell in such a way as to express a fusion protein comprising said CBM. The term thermophilic refers herein to organisms with optimal growth temperature over 40°C. A preferred CBM is coded for by the xylanase10A gene from *Thermotoga maritima*, preferably the region within the host plant or plant cell that codes for a CBM is a region of said gene. Said region coding for a CBM may in certain embodiments comprise a sequence depicted as SEQ ID NO: 1, or a nucleic acid sequence encoding the same amino acid sequence, or a sequence encoding an amino acid sequence with substantial sequence identity to said amino acid sequence.

It may be useful in some embodiments of the invention to heat the protein extract comprising the soluble fusion protein, such as to a temperature in the range of 37°C and 100°C, e.g. a temperature in the range of 50-80°C, for a period of time such as in the range of from 1 min to 120 minutes during the process. For this purpose, heat-stable CBM such as from thermophilic sources is particularly useful. During such heating, a part of the endogenous plant proteins may become inactivated and/or denatured and may thus readily be separated from the protein extract. Said heated extract may preferably be subjected to the process step comprising expanded bed adsorption with a polysaccharide matrix

for the simultaneous separation of solids and affinity binding of said CBM fusion protein from the heated extract.

In particular embodiments of the invention, said heterologous fusion protein comprises a protease (indicating a proteolytically active polypeptide), which in certain useful embodiments is a mammalian enterokinase (EK) or an enterokinase-active part thereof, e.g., a bovine EK or a bovine EK catalytic domain (EKc). A useful EKc for this purpose is encoded for by the nucleic acid sequence shown as SEQ ID NO: 2.

In a highly useful embodiment of the invention, said fusion protein comprises a CBM and a heterologous polypeptide of interest intercepted by a stretch of amino acids comprising a proteolytic cleavage site, preferably a proteolytic cleavage site recognized and cleaved by a specific protease. By having such a site, the CBM can readily be cleaved of the fusion partner in the fusion protein to obtain the desired heterologous protein without the accompanying CBM.

Hence, in a related aspect, the invention provides a process for purification of a heterologous protein of interest, the process comprising

- (a) providing a fusion protein comprising said heterologous protein fused to a CBM as defined herein above, intercepted by a proteolytic cleavage site,
- (a) contacting said fusion protein with a functional protease fused to a CBM , at conditions facilitating proteolytic cleavage by said protease, to cleave the fused CBM from the heterologous protein of interest,
- (b) contacting the solution of CBM-protease, free CBM and heterologous protein of interest to a polysaccharide matrix, such as defined herein, under conditions where the CBM-protease and free CBM binds to said polysaccharide matrix and where the heterologous protein of interest is not retained on said polysaccharide matrix,
- (c) separating the non-bound heterologous protein of interest from the polysaccharide matrix,
- (d) washing the polysaccharide matrix with the bound CBM-protease and CBM, with one or more suitable aqueous solutions,
- (e) eluting the CBM-protease from the matrix by adjusting conditions effecting the release of said CBM-protease off the matrix; and

(f) optionally reconditioning said eluted CBM-protease, to retain its affinity to said polysaccharide matrix, such that the reconditioned CBM-protease can be re-used for subsequent repetition of the process.

5 The steps of binding the fusion protein, washing and eluting are preferably conducted such as described above.

In preferred embodiments, the protease fused to CBM is enterokinase, preferably as described above. Such a CBM-fusion protease, EK or other type, may suitably  
10 be produced and purified by the methods described herein.

It will be appreciated that the method described above may advantageously be combined with the above method to produce and purify a soluble heterologous fusion protein, such as to obtain a desired heterologous protein expressed and  
15 isolated initially as a CBM fusion protein, in a purified form free from the fused CBM.

An additional advantage of the method is the possibility of recycling the protease used, i.e. using the same protease repeatedly for batch production of the desired  
20 protein expressed as a CBM fusion protein, which makes the processes described herein even more economical. This is readily accomplished as the CBM-fused protease is designed without having a proteolytic cleavage site, so as to hinder cleavage of the CBM from the CBM protease.

25 Thus it is a further advantage of the invention that it provides a process enabling recycling of costly, specific proteolytic enzymes, thus additionally improving the economy of affinity purification in downstream processing of heterologous proteins, such as in particular, but not limited to proteins obtained from genetically modified plants, plant derived material and plant cells.

30 The present invention successfully addresses the short-comings of downstream processing involved in of heterologous protein production at large scale, for purposes such as, but not limited to, agriculture, chemical industry and the production of protein-based pharmaceuticals. In particular, it provides a novel  
35 process of separating CBM-fusion proteins from biomass such as plant-derived cellulosic material, with fewer processing steps involved, taking advantage of a safer and more economical affinity chromatography principle amenable for use within the pharmaceutical industry, gentle elution conditions maintaining the

activity of high-value heterologous proteins, and comprising a process step enabling the recycling of a specific high-value protease in the process.

## 5 BRIEF DESCRIPTION OF DRAWINGS

Figure 1 is a schematic diagram of a preferred embodiment of the purification process.

10 Figure 2 demonstrates the results obtained from Example 1 by SDS-PAGE analysis. Lane 1: molecular weight size markers, lane 2: purified CBM9-2, lane 3: washed solids from milled barley seed, lane 4: supernatant after biomass interaction, lane 5: first wash with low salt buffer, lane 6: fifth wash with high salt buffer.

15

## DETAILED DESCRIPTION OF PRESENT INVENTION

Herein below, the present invention will be described in more detail.

20

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood and used by one of skill in the art to which this invention belongs.

25 The term "polypeptide" used herein refers to any polymer of amino acids, being monomeric or multimeric, and does not refer to a specific length of a polymer of amino acids. Thus, for example, the terms peptide, oligopeptide, protein, and enzyme are included within the definition of polypeptide. This term also includes polypeptides with post-expression modifications such as for example,  
30 glycosylations, acetylations, phosphorylations and the like.

The term "heterologous polypeptide of interest" or "polypeptide of interest" used herein refers to any polypeptide intended for expression in plant-cells or plant tissue using the methods or compositions of the present invention. As non-  
35 limiting examples, pharmacological polypeptides (e.g., for medical uses) or industrial polypeptides (e.g. enzymes) can be produced according to the present invention.

The term "downstream processing" refers to the isolation and purification of a biotechnological product to a form suitable for its intended use.

The term "fusion partner" refers herein to a heterologous protein linked to CBM.

5

The term "CBM fusion protein" refers to a molecule consisting of a CBM linked to a heterologous protein, and in the context it is put forward in this invention, a molecule without a proteolytic cleavage site, unless described otherwise.

10 The term "operably linked" refers to a functional linkage between a promoter (nucleic acid expression control sequence, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the promoter directs transcription of the nucleic acid corresponding to the second sequence.

15 The term "denatured" refers to a condition of a protein where the native structure, and consequently the activity of the protein is disrupted, and the protein is unfolded or incorrectly folded changing its native three-dimensional structure.

20 The term "expression" and "production" refer to the biosynthesis of a gene product, including the transcription and translation of said gene product.

"Molecular farming" refers to the operation of using plants of any kind in open fields or in closed facility to express and produce heterologous proteins in their  
25 tissue

The term "transgenic" refers to a any cell, cell line, tissue plant part, organ or organism into which a non-native nucleic acid sequence has been introduced, and therefore altering its genotype, as is progeny thereof in which the non-native  
30 nucleic acid is present. Typically, the non-native nucleic acid sequence was introduced into the genotype by a process of genetic engineering, or was introduced into the genotype of a parent cell or plant by such a process and is subsequently transferred to later generations by sexual crosses or asexual propagation.

35

"Substantial sequence identity" indicates in the context herein at least 50% sequence identity and more preferably at least 60% such at least 70 sequence identity, such as at least 80% and preferably at least 90% sequence identity,

such as at least 95% or 99% sequence identity. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., *J. Mol. Biol.* (1990) 215:403-10. Generally, the default settings with respect to, e.g. "scoring matrix" and "gap penalty" will be used for alignment.

5

The term "transformation" or "transformed" refers to the introduction of a nucleic acid sequence into the DNA genome of a host organism, irrespective of the techniques used for the introduction of the nucleic acid fragment into the host cell.

10

"Thermophilic" refers to an organism with optimal growth temperature over 45°C.

The term "GMP" (good manufacturing practice) dictates the manner in which biopharmaceuticals and other drugs and medical devices are produced. GMP requirements include standard operating procedures, sterile conditions, validation of materials and equipment and trained personnel.

15

Monocotyledonous and dicotyledonous plants that can be genetically manipulated can be used in the present invention. Preferably the plant is a monocotyledonous, more preferably barley, and most preferably the barley *Hordeum vulgare*. A plant that can be genetically transformed is a plant into which non-native DNA sequence, including DNA sequence for a coding region, can be introduced, expressed, stably maintained, and transmitted to subsequent generations of progeny. Genetic manipulation and transformation methods have been used to produce barley plants that are resistant to herbicides including, for instance, bialaphos or basta, or antibiotic, such as hygromycin, as selectable markers.

20

25

## METHODS

30

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

35

Although only preferred embodiments of the invention are specifically illustrated, numerous modifications and variations in the invention as described in the above examples are expected to occur to those skilled in the art, without departing from the spirit and intended scope of the invention.

5

Referring to Fig. 1 illustrating a schematic diagram of the purification process the process can be described as follows:

- 10 (1) The starting material for the process is a transgenic plant, material derived from transgenic plants or transgenic plant cells, including, but not limited to, suspension cultures of plant cells as well as undifferentiated cells of calluses. The material is transgenic in a way that it expresses in a controlled manner a heterologous gene(s) operably linked to a CBM open reading frame, that have been introduced to the
- 15 plant cells through processes known to a person skilled in the art, such as, but not limited to, Agrobacterium-mediated transformation or particle bombardment-mediated transformation or plant viral vector-mediated transformation. The starting material is preferably selected on the basis of satisfactory expression levels of the fusion protein, as deemed by an
- 20 analysis of RNA or protein levels by a person skilled in the art, prior to the initiation of the process described by the invention.
- (2) Disruption of the transgenic material is accomplished by any method known to a person skilled in the art, that results in homogenization of
- 25 the plant tissue and plant cells, in a dry or wetted state. A variety of methods can be chosen from, that suit the source of the plant material. Thus, for seeds, milling is a good way of disrupting the transgenic plant tissue, while for leaves and softer green tissue homogenizing can be accomplished with equipment such as, but not limited to, Waring
- 30 blender, Sorvall Omnimixer or Polytron homogenizers. The equipment for disruption of plant tissue and plant cells is commercially available and easy to scale up as required. General methods of extraction of proteins from plant sources are described by G. Paul Powell in a publication edited by S. Roe, Protein purification applications, 2nd edition (2001). A
- 35 simple and successful method of extraction of soluble proteins from plant sources is the addition of simple buffers like Low salt buffer to the disrupted, homogenized plant tissue, with thorough mixing. Precautions against oxidative tanning, such as addition of polyvinyl pyrrolidine (1%

w/v) are usually sufficient to optimize purification from most plant tissues in order to sequester phenolics from the plant tissue that otherwise could have negative effects on the heterologous protein to be purified. Proteolysis does not always cause problems with plant sources. If, however, proteolysis is a concern, protease inhibitors, such as, e.g., serine-, cysteine- and metalloprotease inhibitors can be added to the extraction buffer. The disruption of the plant material can be done in the presence or absence of a buffered solution. The extraction solution may or may not contain reducing agents such as, but not limited to 2-mercaptoethanol or dithiothreitol (DTT). Soluble plant proteins will be present in the liquid phase together with the CBM-fusion proteins

(3) Mixing of liquid with plant material is essential to extract the water-soluble fusion protein to the liquid phase. The liquid added may or may not contain buffering agents to control pH, preferably within the range of about 5.2 to 8.3, it may or may not contain any reducing agents or sequestering agents as described in (2) accordingly to the protein of interest. In its simplest form, the liquid can be water. After thorough mixing of liquid with the disrupted and homogenized plant material, the liquid phase now contains the CBM-fusion protein.

(4) (A) Depending to some degree on the level of homogenization the mixture of disrupted plant material and extraction liquid can be applied directly to an Expanded Bed Adsorption (EBA) column. In this approach the mixture is applied to the column as a stream of fluid through an expanded bed of affinity adsorption matrix of polysaccharide nature. During the streaming through the column the fusion protein in the liquid phase is exposed to the polysaccharide matrix and is selectively adsorbed through the selective affinity of the CBM to the polysaccharide adsorbent media. Particles such as, but not limited to, cell wall fragments and other solids, together with any soluble plant proteins are flushed through the EBA column in the flow-through liquid.

4(B) Alternatively, a majority of the solids in the mixture can be separated from the liquid prior to the affinity binding step through a variety of methods known to a person skilled in the art, these include, but are not limited to, precipitation, filtration, centrifugation, and sedimentation. As described hereinabove, the solids are discarded and the liquid containing the CBM-fusion protein is subjected to an optional heating step 4(C) or applied directly to the affinity binding step (5).



4(C) Heating of the mixture or liquid prior to affinity step (5) is optional, but may act as an additional purifying step in cases where the CBM-fusion protein as a whole remains soluble at elevated temperatures, while soluble plant proteins may denature and precipitate and endogenous plant proteases may be inactivated through heat. For this purpose, the heating procedure, taking into account the nature of the CBM-fusion protein, may involve heating in the range of 50°C to 100°C, for a period of time in the range of 2 min to 60 minutes during the process. In these embodiments CBM of thermophilic origin are particularly beneficial.

(5) Affinity binding to matrix. The liquid protein extract containing the plant derived CBM-fusion protein is brought into contact with the polysaccharide matrix towards which the CBM has affinity for. The contact can be effected in various ways, such as, but not limited to, chromatography columns packed with the polysaccharide matrix where the liquid is run through the column in either packed or expanded mode, referring to the density of the polysaccharide matrix, or it can be effected in batch mode where the polysaccharide matrix is mixed together with the liquid in a suitable container, with the subsequent recovery of the matrix and the adsorbed CBM-fusion protein. The polysaccharide matrix can be of cellulosic origin such as, but not limited to, Avicel, or it can be of xylanic origin, such as Insoluble xylan. The binding specificity and thermodynamics of CBM9-2 have been studied in detail in a recent publication by Boraston et. al. (2001). It has however surprisingly been found by the present inventors, in contrast to what is indicated in the prior art, that following the methods of the present invention as described herein, CBM9-2 does not bind to plant cell wall components but becomes readily soluble, while retaining good specific binding to a polysaccharide matrix such as used in the affinity adsorption step herein (5). As described herein above this surprising quality introduces several advantages to downstream processing of plant derived CBM-fusion proteins to the extent that a greatly improved downstream processing method is provided.

(6) Washing of the matrix. The polysaccharide affinity adsorbent with CBM-fusion protein bound to it can be washed with several column volumes (relevant quantitative term if the affinity matrix is placed in a chromatography column) of an aqueous solution (e.g. water) or buffer, such as, but not limited to phosphate buffered saline or Tris-based

5 buffers. To improve the efficiency of the washing step, the composition of the washing buffer may be adjusted by means such as, but not limited to, several column volumes of stepwise changes or a gradient of salt concentration or detergent, used to release weakly but nonspecifically bound contaminating proteins from the matrix.

10 (7) Release of fusion protein from matrix. By using CBM-s with the desired binding characteristics as described herein, elution of the CBM-fusion protein from the affinity matrix can be effected with the exposure of the CBM-fusion protein to competing saccharides such as, but not limited to glucose, galactose, lactose, maltose, and cellobiose. Any of these or other similar saccharides, or a combination thereof, can be added in a suitable amount, such as in the range of 1mM to 1 M concentration to an elution buffer such as, e.g., phosphate buffered saline or Tris-based buffers, for the elution step. The saccharide concentration can be e.g. in the range 25 mM to 1 M, such as in the range 50 – 500 mM. These saccharides are commercially available as low-cost bulk chemicals, further improving the overall economy of the downstream processing according to the invention.

20 (8) Isolation/purification of fusion protein. Further purification/isolation of the CBM-fusion protein may be advantageous or required be in some instances. Such further isolation can be accomplished with any of the commonly available chromatographic procedures known to a person skilled in the art, such as, but not limited to, ion exchange chromatography or size exclusion chromatography.

25 (9) Final product. The final product is in this case a CBM-fusion protein in a highly purified form, ready for further formulation and packaging in its final form, if necessary.

30 (10) Isolation of fusion protein containing proteolytic cleavage site. Further isolation of the CBM-fusion protein containing a proteolytic cleavage site may or may not be required or may be advantageous in some instances, before the proteolytic cleavage step (11). This isolation of the fusion protein may also be useful to change the buffer containing the CBM-fusion protein with a proteolytic cleavage site so as to adjust it to conditions favorable for a proteolytic cleavage reaction of step (11).

35 This isolation can be accomplished with any of the commonly available chromatographic procedures known to a person skilled in the art, such as, but not limited to, ion exchange chromatography or size exclusion chromatography.

(11) Proteolytic separation of CBM from heterologous protein fusion partner. At this stage in the process, the CBM-fusion protein containing a proteolytic cleavage site is exposed to a specific protease, fused to CBM but without the cleavage site, which protease is able to recognize the cleavage site and separate the CBM from the heterologous protein of interest. The specific protease linked to CBM is preferably selected from the group of cleavage site-specific proteases, such as enterokinase, Factor Xa, thrombin and the like. After completion of the cleavage reaction, the reaction solution includes released CBM, residual uncleaved CBM-fusion protein, CBM-protease (e.g., CBM-EK), and the released heterologous protein of interest.

(12) Affinity binding of CBM-protease and free CBM to matrix. The solution containing all these components is brought into contact with the polysaccharide matrix which the CBM has affinity for, as described hereinabove in step (5). All CBM-containing components will be adsorbed to the affinity matrix while the released highly purified heterologous protein of interest is recovered in the flow through.

(13) Further isolation of heterologous protein. Although the heterologous protein of interest is already highly purified, further purification/isolation may be required or be advantageous in some instances. This further isolation can be a chromatography step, such as, e.g., ion exchange chromatography or size exclusion chromatography.

(14) Final product. The final product is in this case a heterologous protein in a highly purified form, ready for further formulation (e.g., lyophilization) and packaging in its final form, if necessary.

(15) Washing of the matrix. This step can be performed as described for step (6).

(16) Release of CBM-protease and CBM. Using the elution conditions as described in step (7) above, CBM-protease is brought back in solution. Reconditioning of this solution involves neutralization of conditions and/or removal of the agent(s), (e.g. saccharides) that effected the release of the CBM from the polysaccharide affinity matrix. Said agents can be removed from solution with CBM protease e.g. with ultrafiltration, dialysis, size exclusion chromatography and under certain conditions ion exchange chromatography. Some of these methods such as size exclusion chromatography can in addition purify CBM-protease from residual CBM and CBM-fusion protein, if required.

(17) Recycling of CBM-protease. Once the CBM-protease is reconditioned to a state where it has regained its affinity for said polysaccharide matrix, it can be introduced into the process again for a new round of proteolytic cleavage of CBM-fusion proteins containing proteolytic cleavage site as in step (11). Although the reconstituted CBM-protease solution may contain residual CBM and traces of uncleaved CBM-fusion protein from previous reactions, these will not interfere with the purification of a cleaved heterologous protein fusion partner, as they will co-purify with the CBM-protease. Thus, an efficient recycling of high-value specific CBM-protease improves the efficiency and economy of the novel process of the invention and enables production and purification of recombinantly produced proteins at a large scale, where previously the cost of downstream processing has been prohibitive.

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which is not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

## EXAMPLES

### EXAMPLE 1

#### Biomass interaction study: CBM9-2 and milled barley seed

Dried barley seed was finely ground in a Retsch mill to a fine flour. 1 g of milled seed was used for the extraction of water soluble components from the seed with 5 ml of low salt buffer (50 mM potassium phosphate buffer pH 7.02), as a means to rid the sample of all water soluble components that might interfere with the biomass interaction study. The mixture was vortexed and tumbled for 5 minutes to ensure thorough mixing of the liquid and the milled barley seed material. Following this mixing, the samples were centrifuged at 5000 x g for 4 minutes to pellet the solids. After centrifugation, the supernatant was discarded. This procedure was repeated 3 times with low salt buffer, with the supernatant discarded after each centrifugation. Then the washing procedure was repeated 3

times with high salt buffer (50 mM potassium phosphate buffer pH 7.02, 1 M NaCl), the supernatant discarded as before. The resulting washed solids representing for the most part plant cell-wall fragments and insoluble starch. The washed solids were equilibrated with 3 times washing with low salt buffer as described above, to obtain same conditions that favor affinity binding of CBM9-2 to cellulosic matrix in affinity chromatography. A representative sample of the solids before biomass interaction study was taken for SDS-PAGE analysis (lane 3). 10 µl of bacterially produced CBM9-2 purified on cellulose (Avicel™)-affinity column (O.D. @280 nm 0,394), were taken for later SDS-PAGE (lane 2). The purified CBM9-2 had previously been subjected to repeated (4x) dilution and concentration in a ultrafiltration module as a proven method for desorbing any bound glucose from the CBM9-2, so as to regain the cellulose binding affinity characteristic of the protein.

2 ml of the purified CBM9-2 were added to the washed, equilibrated solids derived from milled barley seed and the mixture incubated while shaking for 60 minutes at room temperature. After incubation, the mixture was spun down at 5000 x g for 10 minutes, and the supernatant subsequently clarified with centrifugation at 13.000 x g for 5 minutes. 10 µl of the clarified supernatant from the biomass interaction was taken for SDS-PAGE analysis (lane 4). Subsequently the pellet consisting of the milled barley seed solids, was washed 5 times with low salt buffer and subsequently 5 times with high salt buffer as described above. 10 µl of the first low salt buffer wash (lane 5) and the fifth low salt buffer wash (lane 6), were prepared for subsequent SDS-PAGE analysis. To elute any bound CBM9-2 from the milled barley seed solids, 1 ml of elution buffer ( ) was added to the solids and incubated during mixing for 15 minutes, before centrifugation at 5000 x g for 5 minutes and removal of the supernatant (eluate). A 10 µl sample of the eluate was prepared for SDS-PAGE analysis (lane 7). A representative sample from the solids after the biomass interaction study and elution was taken for SDS-PAGE analysis (lane 8). The samples from the biomass interaction assay prepared for SDS-PAGE were run on 12.5 % SDS-PAGE gels (PhastGels homogenous 12,5) using PhastSystem (Amersham Pharmacia Biotech). After completion of the run the gel was stained with Coomassie Blue R-250, and destained. The results are illustrated in FIG. 2.

These results demonstrate that CBM9-2 does not bind significantly to plant derived cell-wall fragments or other insoluble solids from milled barley seed.

## EXAMPLE 2

### Purification of CBM9-2 from milled barley seed extract

Barley seeds were milled to finely ground flour using commercially available mill (Aarslev Maskinfabrik, Erhvervsvangen 11, 5792 Aarslev, DK). The resulting barley flour was wetted in Low salt buffer (50 mM potassium phosphate buffer pH 7.02 ) in volume-ratios 2:3, barley flour:buffer, respectively. The liquid was mixed thoroughly with the flour in a vessel and allowed to sediment overnight at 4°C. CBM9-2 purified from bacteria was added to the barley seed-supernatant.

The next day the spiked supernatant (100 ml) containing CBM9-2 was fed to a Streamline 25 (Amersham Biotech) chromatography column containing cellulose (Avicel™). The feed application was done at flowrate 184 cm/h, in expanded bed mode, followed by a washing step with 5 column volumes high salt buffer (1 M NaCl in 50 mM KPO<sub>4</sub>, pH 7.02), followed by 5 column volumes of low salt buffer (50 mM KPO<sub>4</sub>, pH 7.02). The expanded column bed was allowed to sediment (sedimented bed height = 20 cm) and elution was performed at 92 cm/h with 300 ml of elution buffer: 1 M glucose in 50 mM KPO<sub>4</sub>, pH 7.02). The elution conditions resulted in a small peak containing the CBM9-2 protein.

This showed that using the procedure described hereinabove that firstly; CBM9-2 remains in solution unattached to cell-wall fragments and other poorly defined solids from milled barley seed, secondly; it is possible to use polysaccharidic affinity chromatography as described by this invention to capture CBM 9-2 from milled barley-seed extract, thirdly; this can be done by using well defined pharmaceutical grade cellulose (Avicel) as a matrix, and fourthly; the affinity chromatography step can be done in expanded bed mode as described by the invention, fifthly; the CBM9-2 purified from barley seed-extract can be eluted of the matrix under gentle conditions avoiding any denaturing steps, as described by this invention. The very same conditions and procedure as described hereinabove, can be applied to purify CBM9-2-fusion proteins from transgenic milled seed.

The polysaccharidic affinity chromatography described is also valid for the separation of protease-CBM and excised CBM from the protein of interest after a proteolytic cleavage reaction, as described by this invention.

## REFERENCES

Altschul et al., *J. Mol. Biol.* (1990) 215:403-10  
 Boraston et al. (2001) *Biochemistry* 40, pp.6240-6247

- 5 Contributors (2001) in "Recombinant Protein Drugs" Ed. P. Buckel – from series-  
 Milestones in Drug Therapy, Birkhauser Verlag, Basel 2001

Hammond (1999) in "Plant bioechnology; new products and applications" Eds.  
 Hammond, McGarvey & Yusibov, Springer Verlag, NY 1999

- 10 HIC, RPC, IEX, Principles and Methods Series, nr.18-1020-90, nr.18-11134-  
 16, nr.18-1114-21 (respectively) - Amersham Pharmacia Biotech

Kalyanpur M. (2000) in "Downstream processing of proteins" Ed. M.A. Desai  
 Humana Press N.J.

Paul G. Paul Powell G. In "Protein purification applications", Ed. by S.Roe, "2nd  
 edition (2001)

- 15 R.K.Scopes R.K. (1993) in "Protein Purification: Principles and Practice" 3rd  
 ed. Springer-Verlag NY.

Shani et al. US Patent No. 6,331,416

Winterhalter et. al. (1995) *Mol. Microbiol.* 15 (3), 431-444

## CLAIMS

1. A method for production and purification of a soluble heterologous fusion protein comprising a cellulose binding module (CBM), from transgenic plants or transgenic plant cells expressing said fusion protein, comprising
- 5 (a) disrupting the transgenic plant material;
- (b) adding an extraction liquid to the plant material, thereby creating a mixture of soluble and insoluble plant material, so as to extract the soluble fusion protein from said disrupted plant material to the liquid
- 10 phase to obtain a protein extract;
- (c) separating the insoluble plant material, comprising cell-wall material and solids, from said protein extract comprising said fusion protein of interest;
- (d) contacting said protein extract to a polysaccharide matrix which
- 15 binds to said fusion protein;
- (e) washing the matrix with the bound fusion protein with one or more suitable aqueous solutions; and
- (f) eluting the fusion protein from said polysaccharide matrix by
- 20 adjusting conditions effecting the release of said fusion protein from the matrix,
- thereby obtaining the soluble heterologous fusion protein substantially purified.
2. The method of claim 1 wherein said transgenic plant or plant cell is selected from the group of dicotyledonous plants and monocotyledonous plants.
- 25 3. The method of claim 1 wherein said plant cell or transgenic plant is selected from the group of plants including tobacco, rape seed, soy bean, alfalfa, barley, maize, wheat, oat and rice.
- 30 4. The method of claim 1, wherein the separation step (c) comprises a method selected from expanded bed adsorption (EBA), precipitation, filtration, centrifugation, or any combination thereof.



5. The method of claim 1 wherein affinity binding to said polysaccharide matrix in step (d) comprises a chromatography step.
- 5 6. The method of claim 1, combining steps (c) and (d) in a process step comprising expanded bed adsorption with a polysaccharide matrix, as a measure for simultaneous separation of cell-wall material and solids from said protein extract and affinity binding of said CBM-fusion protein onto the polysaccharide matrix.
- 10 7. The method of claim 1, wherein said conditions effecting the elution of said fusion protein from the matrix are non-denaturing conditions that may be neutral or acidic conditions or involve exposure to carbohydrates, or any combination thereof.
- 15 8. The method of claim 1, wherein said polysaccharide matrix comprises cellulose.
9. The method of claim 8, wherein said cellulose matrix comprises a pharmaceutically compatible cellulose.
- 20 10. The method of claim 9, wherein said cellulose is Avicel <sup>TM</sup>.
11. The method of claim 1, wherein said transgenic plant or plant cell comprises a nucleic acid sequence encoding for a CBM.
- 25 12. The method of claim 11, wherein said CBM is heat-stable and remains soluble at elevated temperatures.
13. The method of claim 12, wherein said region coding for a CBM is a region of the xylanase10A gene from *Thermotoga maritima*.
- 30 14. The method of claim 13, wherein said region coding for a CBM comprises a sequence depicted as SEQ ID NO: 1, or a sequence encoding the same

amino acid sequence or an amino acid sequence with substantial sequence identity to said sequence.

- 5 15. The method of claim 1, wherein said protein extract is heated to a temperature in the range of 37°C and 100°C, for a period of time in the range of from 1 min to 120 minutes during the process.
- 10 16. The method of claim 16, wherein said heated extract is subjected to the process step comprising expanded bed adsorption with a polysaccharide matrix for the simultaneous separation of solids and affinity binding of said CBM fusion protein from the heated extract.
- 15 17. The method of claim 1, wherein said heterologous fusion protein comprises a protease.
18. The method of claim 18, wherein said protease is mammalian enterokinase (EK) or an enterokinase active part thereof.
- 20 19. The method of claim 19, wherein said EK comprises a bovine EK catalytic domain (EKc).
20. The method of claim 20, wherein said bovine EKc is encoded by the nucleic acid sequence shown as SEQ ID NO: 2.
- 25 21. The method of claim 1, wherein said fusion protein comprises a CBM and a heterologous polypeptide of interest intercepted by a proteolytic cleavage site.
- 30 22. A process for purification of a heterologous protein of interest, comprising
- (a) providing a fusion protein comprising said heterologous protein fused to a CBM intercepted by a proteolytic cleavage site,
- 35 (b) contacting said fusion protein with a functional protease fused to a CBM , at conditions facilitating proteolytic cleavage by said protease, to cleave the CBM from the heterologous protein of interest,

- (c) contacting the solution of CBM-protease, free CBM and heterologous protein of interest to a polysaccharide matrix, under conditions where the CBM-protease and free CBM binds to said polysaccharide matrix and where the heterologous protein of interest is not retained on said polysaccharide matrix,
- (d) separating the non-bound heterologous protein of interest from the polysaccharide matrix,
- (e) washing the polysaccharide matrix with the bound CBM-protease and CBM, with one or more suitable aqueous solutions,
- (f) eluting the CBM-protease from the matrix by adjusting conditions effecting the release of said CBM-protease off the matrix; and
- (g) optionally reconditioning said eluted CBM-protease, to retain its affinity to said polysaccharide matrix, such that the reconditioned CBM-protease can be re-used for subsequent repetition of the process defined by steps (a) – (f).

23. The process of claim 23, wherein said protease fused to CBM is enterokinase.

24. The process of claim 23, wherein said protease fused to CBM is obtained by the method of claim 1.

25. The process of claim 23, wherein said polysaccharide matrix comprises cellulose.

26. The process of claim 26, wherein said cellulose is a pharmaceutically compatible cellulose.

27. The process of claim 26, wherein said cellulose is Avicel™.

28. The process of claim 23, wherein said reconditioning of the eluted CBM-protease involves neutralization, and/or removal from the CBM-protease eluent of agents that affect the release of CBM from said polysaccharide matrix.

29. The method of claim 28, wherein said reconditioning comprises neutralization or removal from the eluent of carbohydrates such as saccharides.

## ABSTRACT

5 The present invention relates to improved methods for protein purification of high-value heterologous proteins produced in plants, plant derived tissue or plant cells. The invention aims to reduce the cost and improve the quality of downstream processing of heterologous proteins produced in plants.

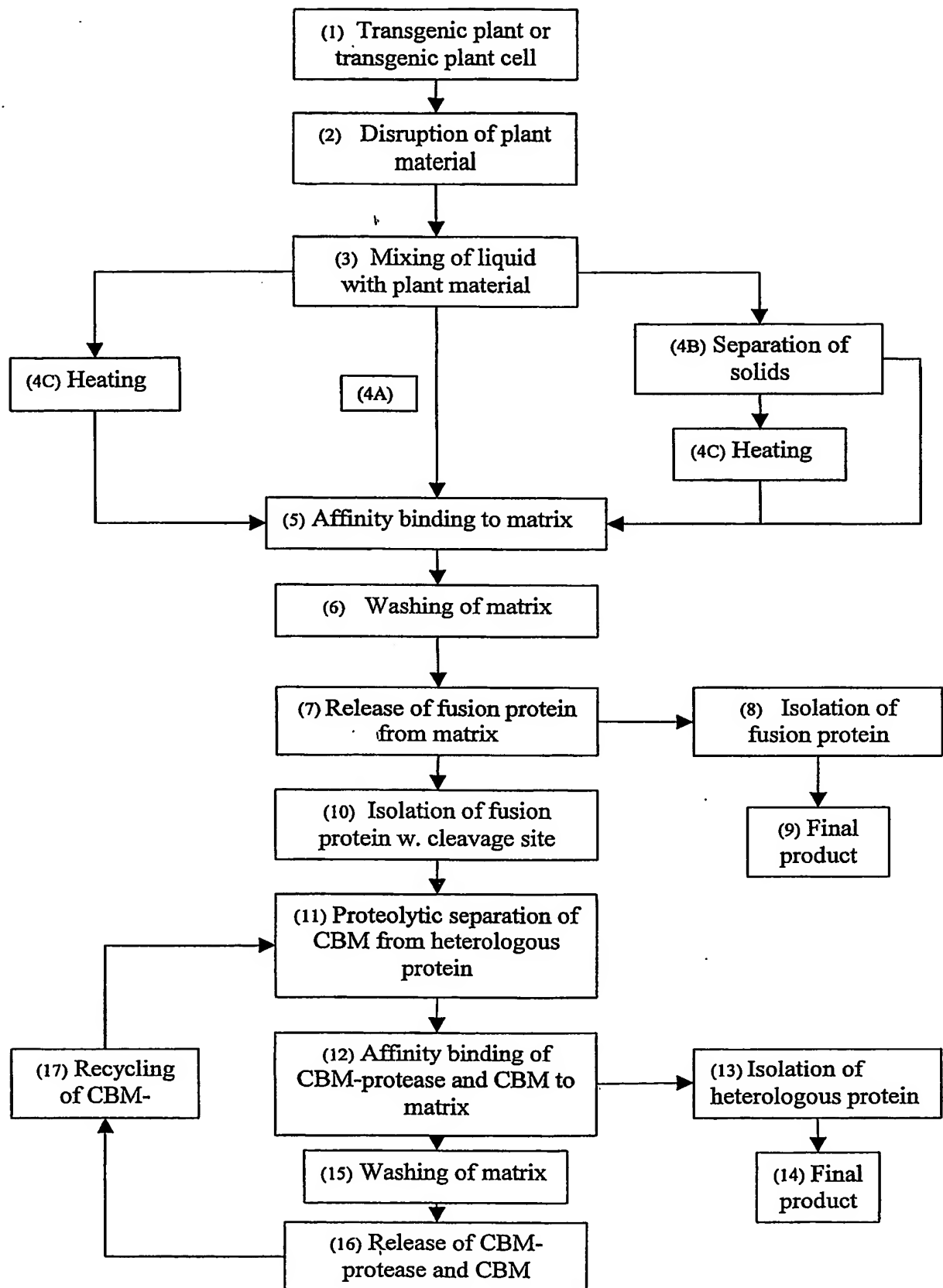
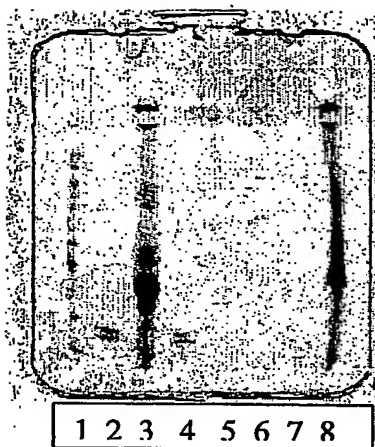


Fig. 1



**Fig. 2**

BEST AVAILABLE COPY